



CPI-004DVCP3CN

SEQUENCE LISTING

<110> Johnson, Gary L.

<120> Method And Product For Regulating Cell Responsiveness To External Signals

<130> CPI-004DVCP3CN

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<150> 09/608,890

<151> 2000-30-06

<150> 08/440,421

<151> 1995-05-15

<150> 08/323,460

<151> 1994-10-14

<150> 08/049,254

<151> 1993-04-15

<150> 08/410,602

<151> 1995-03-24

<150> 08/472,934

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<170> PatentIn Ver. 2.0

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NOV 24 2004

TECH CENTER 1600/2900

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 Ser Gly Phe Pro Gly Ala Ala Ala Ala Ser Pro Glu Ala Gly Gly Gly
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Lys Gly Ala Asn Ile Leu Arg Asp Ser Thr Gly Asn Ile Lys Leu Gly	
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gac ttt ggg gct agt aaa cgg ctt cag acc atc tgt ctc tca ggc aca	2013
Asp Phe Gly Ala Ser Lys Arg Leu Gln Thr Ile Cys Leu Ser Gly Thr	
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Gly Met Lys Ser Val Thr Gly Thr Pro Tyr Trp Met Ser Pro Glu Val	
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Ile Ser Gly Glu Gly Tyr Gly Arg Lys Ala Asp Ile Trp Ser Val Ala	
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Cys Thr Val Val Glu Met Leu Thr Glu Lys Pro Pro Trp Ala Glu Phe	
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Glu Ala Met Ala Ala Ile Phe Lys Ile Ala Thr Gln Pro Thr Asn Pro	
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Lys Leu Pro Pro His Val Ser Asp Tyr Thr Arg Asp Phe Leu Lys Arg	
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Ile Phe Val Glu Ala Lys Leu Arg Pro Ser Ala Glu Glu Leu Leu Arg	
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His Met Phe Val His Tyr His	
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 Glu His Arg Gly Glu Lys Arg Ile Leu Gln Val Thr Arg Pro Val Lys
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 Asp Leu His Tyr Thr Asn Asn Glu Leu Val Ile Pro Leu Thr Thr Gln
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 Asp Asp Leu Asp Lys Ala Val Glu Leu Leu Asp Arg Ser Ile His Met
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 Gly Ala Glu Arg Lys Lys Arg Leu Ser Val Val Gly Pro Pro Asn Arg
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 Asp Arg Ser Ser Pro Pro Gly Tyr Ile Pro Asp Ile Leu His Gln
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 Pro Glu Asn Ser Gly Ser Gly Ser Cys Pro Ser Leu Asp Ser Pro Leu
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 Asp Gly Glu Ser Tyr Pro Lys Ser Arg Met Pro Arg Ala Gln Ser Tyr
 225 230 235 240
 Pro Asp Asn His Gln Glu Phe Thr Asp Tyr Asp Asn Pro Ile Phe Glu
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 Lys Phe Gly Lys Gly Gly Thr Tyr Pro Arg Arg Tyr His Val Ser Tyr
 260 265 270
 His His Gln Glu Tyr Asn Asp Gly Arg Lys Thr Phe Pro Arg Ala Arg
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 Arg Thr Gln Gly Thr Ser Phe Arg Ser Pro Val Ser Phe Ser Pro Thr

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Asp His Ser Leu Ser Thr Ser Ser Gly Ser Ser Val Phe Thr Pro Glu 305 310 315 320		
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Arg Val Tyr Leu Cys Tyr Asp Val Asp Thr Gly Arg Glu Leu Ala Val 370 375 380		
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Asn Ala Leu Glu Cys Glu Ile Gln Leu Leu Lys Asn Leu Leu His Glu 405 410 415		
Arg Ile Val Gln Tyr Tyr Gly Cys Leu Arg Asp Pro Gln Glu Lys Thr 420 425 430		
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Leu Lys Ala Tyr Gly Ala Leu Thr Glu Asn Val Thr Arg Lys Tyr Thr 450 455 460		
Arg Gln Ile Leu Glu Gly Val His Tyr Leu His Ser Asn Met Ile Val 465 470 475 480		
His Arg Asp Ile Lys Gly Ala Asn Ile Leu Arg Asp Ser Thr Gly Asn 485 490 495		
Ile Lys Leu Gly Asp Phe Gly Ala Ser Lys Arg Leu Gln Thr Ile Cys 500 505 510		
Leu Ser Gly Thr Gly Met Lys Ser Val Thr Gly Thr Pro Tyr Trp Met 515 520 525		
Ser Pro Glu Val Ile Ser Gly Glu Gly Tyr Gly Arg Lys Ala Asp Ile 530 535 540		
Trp Ser Val Ala Cys Thr Val Val Glu Met Leu Thr Glu Lys Pro Pro 545 550 555 560		
Trp Ala Glu Phe Glu Ala Met Ala Ala Ile Phe Lys Ile Ala Thr Gln 565 570 575		
Pro Thr Asn Pro Lys Leu Pro Pro His Val Ser Asp Tyr Thr Arg Asp 580 585 590		
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Ala Leu Asp Ser Ile Met Lys Asp Leu Val Ala Leu Gln Met Ser Arg
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Arg Thr Arg Leu Ser Gly Tyr Glu Thr Met Lys Asn Lys Asp Thr Gly
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gag aga cga att ata gca ttc agc cgg cct gtg aga tac gaa gat gtg      606
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aaa gcc att gac att ttg gat aga agc tca agt atg aaa agc ctt agg      750
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ata cta ctg tta tcc caa gac aga aac cat act agt tcc tct ccc cac      798
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Ser Val Ser Ser Gln Asn Pro Gly Arg Ser Ser Pro Pro Pro Gly Tyr
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gta cct gag cga caa cag cac att gcc cgg caa gga tcc tat acg agc      990
Val Pro Glu Arg Gln Gln His Ile Ala Arg Gln Gly Ser Tyr Thr Ser
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Leu	Asp	Leu	His	Tyr	Met	Asn	Asn	Glu	Leu	Ser	Ile	Leu	Leu	Lys	Asn
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Gln	Asp	Asp	Leu	Asp	Lys	Ala	Ile	Asp	Ile	Leu	Asp	Arg	Ser	Ser	Ser
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Arg	Lys	Ser	Gln	Met	Ser	Arg	Ala	Arg	Ser	Phe	Pro	Asp	Asn	Arg	Lys
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Glu	Cys	Ser	Asp	Arg	Glu	Thr	Gln	Leu	Tyr	Asp	Lys	Gly	Val	Lys	Gly
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Gly	Thr	Tyr	Pro	Arg	Arg	Tyr	His	Val	Ser	Val	His	His	Lys	Asp	Tyr
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Leu	Phe	Thr	Leu	Val	Pro	Ser	Ser	Arg	Ser	Leu	Ser	Thr	Asn	Gly	Glu
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Asn Met Gly Val Ala Val Gln Tyr Leu Asp Pro Arg Gly Arg Leu Arg
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 Ser Ala Asp Ser Glu Asn Ala Leu Thr Val Gln Glu Arg Asn Val Pro
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 Gly Arg Glu Leu Ala Ser Lys Gln Val Gln Phe Asp Pro Asp Ser Pro
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 Lys Asn Leu Gln His Glu Arg Ile Val Gln Tyr Tyr Gly Cys Leu Arg
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 Asp Arg Ala Glu Lys Ile Leu Thr Ile Phe Met Glu Tyr Met Pro Gly
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 Gly Ser Val Lys Asp Gln Leu Lys Ala Tyr Gly Ala Leu Thr Glu Ser
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His Tyr Ile Arg Gly Gly Glu Ala Gln Ala Gly Lys Leu Phe Cys Asp
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Leu Gln Glu Ser Cys Ala Glu Leu Trp Thr Xaa Ala Asp Asp Asn Gly
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aag gag ctc ttc cac gaa gcc agg gaa aga gcc tcc aag gcc ctg ggc 1205

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Pro	Asp	Ser	Leu	Ala	Glu	Glu	Lys	Lys	Ile	Ile	Leu	Gln	Leu	Leu	Asn		
			205					210					215				
gct	gcc	aca	gga	aag	gac	tgc	tca	aag	gat	cca	gac	gac	gtc	ttc	atg	1445	
Ala	Ala	Thr	Gly	Lys	Asp	Cys	Ser	Lys	Asp	Pro	Asp	Asp	Val	Phe	Met		
		220					225					230					
gat	gcc	ttc	ctg	ctc	ctg	acc	aag	cat	ggg	gac	cga	gcc	cgt	gac	tca	1493	
Asp	Ala	Phe	Leu	Leu	Leu	Thr	Lys	His	Gly	Asp	Arg	Ala	Arg	Asp	Ser		
		235				240					245						
gaa	gat	ggc	tgg	ggc	aca	tgg	gaa	gct	cgg	gct	gtc	aaa	att	gtg	cct	1541	
Glu	Asp	Gly	Trp	Gly	Thr	Trp	Glu	Ala	Arg	Ala	Val	Lys	Ile	Val	Pro		
		250			255				260						265		
cag	gtg	gag	act	gtg	gac	acc	ctg	aga	agc	atg	cag	gtg	gac	aac	ctt	1589	
Gln	Val	Glu	Thr	Val	Asp	Thr	Leu	Arg	Ser	Met	Gln	Val	Asp	Asn	Leu		
				270					275					280			
ctg	ctg	gtt	gtc	atg	gag	tct	gct	cac	ctc	gta	ctt	cag	aga	aaa	gcc	1637	
Leu	Leu	Val	Val	Met	Glu	Ser	Ala	His	Leu	Val	Leu	Gln	Arg	Lys	Ala		
			285					290					295				
ttc	cag	cag	tcc	att	gag	ggg	ctg	atg	act	gta	cgc	cat	gag	cag	aca	1685	
Phe	Gln	Gln	Ser	Ile	Glu	Gly	Leu	Met	Thr	Val	Arg	His	Glu	Gln	Thr		
		300					305					310					
tct	agc	cag	ccc	atc	atc	gcc	aaa	ggg	ttg	cag	cag	ctc	aag	aac	gat	1733	
Ser	Ser	Gln	Pro	Ile	Ile	Ala	Lys	Gly	Leu	Gln	Gln	Leu	Lys	Asn	Asp		
		315				320					325						
gca	ctt	gag	cta	tgc	aac	aga	atc	agc	gat	gcc	atc	gac	cgt	gtg	gac	1781	
Ala	Leu	Glu	Leu	Cys	Asn	Arg	Ile	Ser	Asp	Ala	Ile	Asp	Arg	Val	Asp		
				335						340					345		
cac	atg	ttc	acc	ctg	gag	ttc	gat	gct	gag	gtc	gag	gag	tct	gag	tcg	1829	
His	Met	Phe	Thr	Leu	Glu	Phe	Asp	Ala	Glu	Val	Glu	Glu	Ser	Glu	Ser		
				350					355					360			
gcc	acg	ctg	cag	cag	tac	tac	cga	gaa	gcc	atg	att	cag	ggc	tac	aac	1877	
Ala	Thr	Leu	Gln	Gln	Tyr	Tyr	Arg	Glu	Ala	Met	Ile	Gln	Gly	Tyr	Asn		
			365					370					375				
ttt	ggg	ttt	gag	tat	cat	aaa	gaa	gtt	gtt	cgt	ttg	atg	tct	ggg	gaa	1925	
Phe	Gly	Phe	Glu	Tyr	His	Lys	Glu	Val	Val	Arg	Leu	Met	Ser	Gly	Glu		
		380					385					390					
ttc	agg	cag	aag	ata	gga	gac	aaa	tat	ata	acg	ttc	gcc	cag	aag	tgg	1973	
Phe	Arg	Gln	Lys	Ile	Gly	Asp	Lys	Tyr	Ile	Thr	Phe	Ala	Gln	Lys	Trp		
		395				400					405						
atg	aat	tac	gtg	ctg	acc	aaa	tgc	gag	agc	ggc	aga	ggc	aca	aga	ccc	2021	

Met	Asn	Tyr	Val	Leu	Thr	Lys	Cys	Glu	Ser	Gly	Arg	Gly	Thr	Arg	Pro	
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aga	tgg	gcc	acc	caa	gga	ttt	gat	ttc	cta	caa	gcc	att	gaa	cct	gcc	2069
Arg	Trp	Ala	Thr	Gln	Gly	Phe	Asp	Phe	Leu	Gln	Ala	Ile	Glu	Pro	Ala	
				430					435					440		
ttt	att	tca	gct	tta	cca	gaa	gat	gac	ttc	ttg	agt	ttg	caa	gcc	ctg	2117
Phe	Ile	Ser	Ala	Leu	Pro	Glu	Asp	Asp	Phe	Leu	Ser	Leu	Gln	Ala	Leu	
			445					450					455			
atg	aat	gag	tgc	atc	ggg	cac	gtc	ata	gga	aag	cca	cac	agc	cct	gtc	2165
Met	Asn	Glu	Cys	Ile	Gly	His	Val	Ile	Gly	Lys	Pro	His	Ser	Pro	Val	
		460					465					470				
aca	gct	atc	cat	cgg	aac	agc	ccc	cgc	cct	gtg	aag	gtg	ccc	cga	tgc	2213
Thr	Ala	Ile	His	Arg	Asn	Ser	Pro	Arg	Pro	Val	Lys	Val	Pro	Arg	Cys	
	475					480					485					
cac	agt	gac	cct	cct	aac	cct	cac	ctc	atc	atc	ccg	act	cca	gag	gga	2261
His	Ser	Asp	Pro	Pro	Asn	Pro	His	Leu	Ile	Ile	Pro	Thr	Pro	Glu	Gly	
490					495					500					505	
ttc	agg	ggt	tcc	agt	gtc	cct	gaa	aac	gac	cgc	ttg	gcc	tcc	ata	gct	2309
Phe	Arg	Gly	Ser	Ser	Val	Pro	Glu	Asn	Asp	Arg	Leu	Ala	Ser	Ile	Ala	
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gca	gaa	ctg	cag	ttc	agg	tct	ctg	agt	cgg	cac	tca	agc	ccc	acg	gaa	2357
Ala	Glu	Leu	Gln	Phe	Arg	Ser	Leu	Ser	Arg	His	Ser	Ser	Pro	Thr	Glu	
			525					530					535			
gag	cga	gac	gag	cca	gcg	tat	cct	cgg	agt	gac	tca	agt	gga	tca	act	2405
Glu	Arg	Asp	Glu	Pro	Ala	Tyr	Pro	Arg	Ser	Asp	Ser	Ser	Gly	Ser	Thr	
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cgg	aga	agc	tgg	gaa	ctt	cga	aca	ctc	atc	agc	cag	acc	aaa	gac	tcg	2453
Arg	Arg	Ser	Trp	Glu	Leu	Arg	Thr	Leu	Ile	Ser	Gln	Thr	Lys	Asp	Ser	
	555					560					565					
gcc	tct	aag	cag	ggg	ccc	ata	gaa	gct	atc	cag	aag	tca	gtc	cga	ctg	2501
Ala	Ser	Lys	Gln	Gly	Pro	Ile	Glu	Ala	Ile	Gln	Lys	Ser	Val	Arg	Leu	
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Phe	Glu	Glu	Arg	Arg	Tyr	Arg	Glu	Met	Arg	Arg	Lys	Asn	Ile	Ile	Gly	
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caa	gtg	tgc	gat	acc	cct	aag	tcc	tat	gat	aac	gtc	atg	cat	gtt	gga	2597
Gln	Val	Cys	Asp	Thr	Pro	Lys	Ser	Tyr	Asp	Asn	Val	Met	His	Val	Gly	
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ctg	agg	aag	gtg	aca	ttt	aag	tgg	caa	aga	gga	aac	aaa	att	gga	gaa	2645
Leu	Arg	Lys	Val	Thr	Phe	Lys	Trp	Gln	Arg	Gly	Asn	Lys	Ile	Gly	Glu	
		620					625					630				
gga	cag	tat	gga	aaa	gta	tac	acc	tgc	atc	agt	gtt	gac	aca	ggg	gag	2693
Gly	Gln	Tyr	Gly	Lys	Val	Tyr	Thr	Cys	Ile	Ser	Val	Asp	Thr	Gly	Glu	
	635					640					645					
ctg	atg	gcc	atg	aag	gag	att	cga	ttt	cag	cct	aac	gac	cac	aag	act	2741
Leu	Met	Ala	Met	Lys	Glu	Ile	Arg	Phe	Gln	Pro	Asn	Asp	His	Lys	Thr	
					655					660					665	
atc	aag	gag	act	gca	gac	gag	ttg	aaa	ata	ttt	gaa	ggc	atc	aag	cac	2789
Ile	Lys	Glu	Thr	Ala	Asp	Glu	Leu	Lys	Ile	Phe	Glu	Gly	Ile	Lys	His	
				670					675					680		
ccc	aac	ctg	gtc	cgg	tat	ttt	ggc	gtg	gag	ctt	cac	agg	gaa	gag	atg	2837

Pro	Asn	Leu	Val	Arg	Tyr	Phe	Gly	Val	Glu	Leu	His	Arg	Glu	Glu	Met	
			685					690					695			
tac	atc	ttc	atg	gag	tac	tgt	gat	gag	ggg	aca	cta	gag	gag	gtg	tca	2885
Tyr	Ile	Phe	Met	Glu	Tyr	Cys	Asp	Glu	Gly	Thr	Leu	Glu	Glu	Val	Ser	
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cga	ctg	ggc	ctg	cag	gag	cac	gtc	atc	agg	tta	tat	acc	aag	cag	atc	2933
Arg	Leu	Gly	Leu	Gln	Glu	His	Val	Ile	Arg	Leu	Tyr	Thr	Lys	Gln	Ile	
	715					720					725					
act	gtc	gcc	atc	aac	gtc	ctc	cat	gag	cac	ggc	atc	gtt	cac	cga	gac	2981
Thr	Val	Ala	Ile	Asn	Val	Leu	His	Glu	His	Gly	Ile	Val	His	Arg	Asp	
	730				735					740					745	
atc	aaa	ggg	gcc	aat	atc	ttc	ctt	acg	tca	tct	gga	cta	atc	aag	ctg	3029
Ile	Lys	Gly	Ala	Asn	Ile	Phe	Leu	Thr	Ser	Ser	Gly	Leu	Ile	Lys	Leu	
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gga	gat	ttt	gga	tgc	tct	gta	aaa	ctt	aaa	aac	aac	gcc	cag	acc	atg	3077
Gly	Asp	Phe	Gly	Cys	Ser	Val	Lys	Leu	Lys	Asn	Asn	Ala	Gln	Thr	Met	
			765					770					775			
ccc	gga	gag	gtg	aac	agc	acc	cta	ggg	aca	gca	gct	tac	atg	gcc	cct	3125
Pro	Gly	Glu	Val	Asn	Ser	Thr	Leu	Gly	Thr	Ala	Ala	Tyr	Met	Ala	Pro	
		780					785						790			
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Glu	Val	Ile	Thr	Arg	Ala	Lys	Gly	Glu	Gly	His	Gly	Arg	Ala	Ala	Asp	
	795					800					805					
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Ile	Trp	Ser	Leu	Gly	Cys	Val	Val	Ile	Glu	Met	Val	Thr	Gly	Lys	Arg	
	810				815					820					825	
cct	tgg	cat	gag	tat	gaa	cac	aac	ttt	cag	att	atg	tac	aag	gtg	ggg	3269
Pro	Trp	His	Glu	Tyr	Glu	His	Asn	Phe	Gln	Ile	Met	Tyr	Lys	Val	Gly	
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Met	Gly	His	Lys	Pro	Pro	Ile	Pro	Glu	Arg	Leu	Ser	Pro	Glu	Gly	Lys	
			845					850					855			
gcc	ttt	ctc	tgc	cac	tgc	ctg	gaa	agt	gac	ccg	aag	ata	cgg	tgg	aca	3365
Ala	Phe	Leu	Ser	His	Cys	Leu	Glu	Ser	Asp	Pro	Lys	Ile	Arg	Trp	Thr	
		860					865					870				
gcc	agc	cag	ctc	ctc	gac	cac	gct	ttt	gtc	aag	gtt	tgc	aca	gat	gaa	3413
Ala	Ser	Gln	Leu	Leu	Asp	His	Ala	Phe	Val	Lys	Val	Cys	Thr	Asp	Glu	
	875					880				885						
gag	tgaagtgaac	cagtcctgtg	cctagtagtg	tgtggacaga	atcccgtgat											3466
Glu																
	890															
cactactgta	tgtaatat	acataaagac	tgcagcgag	gcggccttcc	taacctccca											3526
ggactgaaga	ctacaggggt	gacaagcctc	acttctgctg	ctcctgtcgc	ctgctgagtg											3586
acagtgtga	gggttaaagga	gccgcacgtt	aagtgccatt	actactgtac	acggccaccg											3646
cctctgtccc	ctccgaccct	ctcgtgactg	agaaccaacc	gtgtcatcag	cacagtgttt											3706
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3913

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<211> 890

<212> PRT

<213> Mus musculus

<220>

<223> At position 116, Xaa = any amino acid

<400> 12

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Met	Leu	Met	Val	Tyr	Phe	Asp	Tyr	Met	Arg	Ser	Trp	Ile	Gln	Met	Leu
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Gln	Gln	Leu	Pro	Gln	Ala	Ser	His	Ser	Leu	Lys	Asn	Leu	Leu	Glu	Glu
	50					55					60				

Glu	Trp	Asn	Phe	Thr	Lys	Glu	Ile	Thr	His	Tyr	Ile	Arg	Gly	Gly	Glu
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Ala	Gln	Ala	Gly	Lys	Leu	Phe	Cys	Asp	Ile	Ala	Gly	Met	Leu	Leu	Lys
				85					90					95	

Ser	Thr	Gly	Ser	Phe	Leu	Glu	Ser	Gly	Leu	Gln	Glu	Ser	Cys	Ala	Glu
			100					105					110		

Leu	Trp	Thr	Xaa	Ala	Asp	Asp	Asn	Gly	Ala	Ala	Asp	Glu	Leu	Arg	Arg
		115					120					125			

Ser	Val	Ile	Glu	Ile	Ser	Arg	Ala	Leu	Lys	Glu	Leu	Phe	His	Glu	Ala
	130					135					140				

Arg	Glu	Arg	Ala	Ser	Lys	Ala	Leu	Gly	Phe	Ala	Lys	Met	Leu	Arg	Lys
145					150					155					160

Asp	Leu	Glu	Ile	Ala	Ala	Glu	Phe	Val	Leu	Ser	Ala	Ser	Ala	Arg	Glu
				165				170						175	

Leu	Leu	Asp	Ala	Leu	Lys	Ala	Lys	Gln	Tyr	Val	Lys	Val	Gln	Ile	Pro
		180						185					190		

Gly	Leu	Glu	Asn	Leu	His	Val	Phe	Val	Pro	Asp	Ser	Leu	Ala	Glu	Glu
		195					200					205			

Lys	Lys	Ile	Ile	Leu	Gln	Leu	Leu	Asn	Ala	Ala	Thr	Gly	Lys	Asp	Cys
	210					215					220				

Ser	Lys	Asp	Pro	Asp	Asp	Val	Phe	Met	Asp	Ala	Phe	Leu	Leu	Leu	Thr
225					230					235					240

Lys	His	Gly	Asp	Arg	Ala	Arg	Asp	Ser	Glu	Asp	Gly	Trp	Gly	Thr	Trp
				245					250					255	

Glu	Ala	Arg	Ala	Val	Lys	Ile	Val	Pro	Gln	Val	Glu	Thr	Val	Asp	Thr
			260					265					270		

Leu	Arg	Ser	Met	Gln	Val	Asp	Asn	Leu	Leu	Leu	Val	Val	Met	Glu	Ser
		275					280					285			

Ala His Leu Val Leu Gln Arg Lys Ala Phe Gln Gln Ser Ile Glu Gly
 290 295 300
 Leu Met Thr Val Arg His Glu Gln Thr Ser Ser Gln Pro Ile Ile Ala
 305 310 315 320
 Lys Gly Leu Gln Gln Leu Lys Asn Asp Ala Leu Glu Leu Cys Asn Arg
 325 330 335
 Ile Ser Asp Ala Ile Asp Arg Val Asp His Met Phe Thr Leu Glu Phe
 340 345 350
 Asp Ala Glu Val Glu Glu Ser Glu Ser Ala Thr Leu Gln Gln Tyr Tyr
 355 360 365
 Arg Glu Ala Met Ile Gln Gly Tyr Asn Phe Gly Phe Glu Tyr His Lys
 370 375 380
 Glu Val Val Arg Leu Met Ser Gly Glu Phe Arg Gln Lys Ile Gly Asp
 385 390 395 400
 Lys Tyr Ile Thr Phe Ala Gln Lys Trp Met Asn Tyr Val Leu Thr Lys
 405 410 415
 Cys Glu Ser Gly Arg Gly Thr Arg Pro Arg Trp Ala Thr Gln Gly Phe
 420 425 430
 Asp Phe Leu Gln Ala Ile Glu Pro Ala Phe Ile Ser Ala Leu Pro Glu
 435 440 445
 Asp Asp Phe Leu Ser Leu Gln Ala Leu Met Asn Glu Cys Ile Gly His
 450 455 460
 Val Ile Gly Lys Pro His Ser Pro Val Thr Ala Ile His Arg Asn Ser
 465 470 475 480
 Pro Arg Pro Val Lys Val Pro Arg Cys His Ser Asp Pro Pro Asn Pro
 485 490 495
 His Leu Ile Ile Pro Thr Pro Glu Gly Phe Arg Gly Ser Ser Val Pro
 500 505 510
 Glu Asn Asp Arg Leu Ala Ser Ile Ala Ala Glu Leu Gln Phe Arg Ser
 515 520 525
 Leu Ser Arg His Ser Ser Pro Thr Glu Glu Arg Asp Glu Pro Ala Tyr
 530 535 540
 Pro Arg Ser Asp Ser Ser Gly Ser Thr Arg Arg Ser Trp Glu Leu Arg
 545 550 555 560
 Thr Leu Ile Ser Gln Thr Lys Asp Ser Ala Ser Lys Gln Gly Pro Ile
 565 570 575
 Glu Ala Ile Gln Lys Ser Val Arg Leu Phe Glu Glu Arg Arg Tyr Arg
 580 585 590
 Glu Met Arg Arg Lys Asn Ile Ile Gly Gln Val Cys Asp Thr Pro Lys
 595 600 605
 Ser Tyr Asp Asn Val Met His Val Gly Leu Arg Lys Val Thr Phe Lys
 610 615 620
 Trp Gln Arg Gly Asn Lys Ile Gly Glu Gly Gln Tyr Gly Lys Val Tyr
 625 630 635 640
 Thr Cys Ile Ser Val Asp Thr Gly Glu Leu Met Ala Met Lys Glu Ile
 645 650 655

Arg Phe Gln Pro Asn Asp His Lys Thr Ile Lys Glu Thr Ala Asp Glu
 660 665 670
 Leu Lys Ile Phe Glu Gly Ile Lys His Pro Asn Leu Val Arg Tyr Phe
 675 680 685
 Gly Val Glu Leu His Arg Glu Glu Met Tyr Ile Phe Met Glu Tyr Cys
 690 695 700
 Asp Glu Gly Thr Leu Glu Glu Val Ser Arg Leu Gly Leu Gln Glu His
 705 710 715 720
 Val Ile Arg Leu Tyr Thr Lys Gln Ile Thr Val Ala Ile Asn Val Leu
 725 730 735
 His Glu His Gly Ile Val His Arg Asp Ile Lys Gly Ala Asn Ile Phe
 740 745 750
 Leu Thr Ser Ser Gly Leu Ile Lys Leu Gly Asp Phe Gly Cys Ser Val
 755 760 765
 Lys Leu Lys Asn Asn Ala Gln Thr Met Pro Gly Glu Val Asn Ser Thr
 770 775 780
 Leu Gly Thr Ala Ala Tyr Met Ala Pro Glu Val Ile Thr Arg Ala Lys
 785 790 795 800
 Gly Glu Gly His Gly Arg Ala Ala Asp Ile Trp Ser Leu Gly Cys Val
 805 810 815
 Val Ile Glu Met Val Thr Gly Lys Arg Pro Trp His Glu Tyr Glu His
 820 825 830
 Asn Phe Gln Ile Met Tyr Lys Val Gly Met Gly His Lys Pro Pro Ile
 835 840 845
 Pro Glu Arg Leu Ser Pro Glu Gly Lys Ala Phe Leu Ser His Cys Leu
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 Ala Phe Val Lys Val Cys Thr Asp Glu Glu
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 gcacgg atg aga gac gcc atc gcc gag ccg gtg ccc cct cct gcc ctc 168
 Met Arg Asp Ala Ile Ala Glu Pro Val Pro Pro Pro Ala Leu
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 gcc gac acc cct gca gcc gcc atg gag gag ctg cgg cca gca ccg ccg 216
 Ala Asp Thr Pro Ala Ala Ala Met Glu Glu Leu Arg Pro Ala Pro Pro
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cca cag ccc gag ccg gat ccg gag tgc tgc cca gcg gcg agg cag gag	264
Pro Gln Pro Glu Pro Asp Pro Glu Cys Cys Pro Ala Ala Arg Gln Glu	
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Cys Met Leu Gly Glu Ser Ala Arg Lys Ser Met Glu Ser Asp Pro Glu	
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gac ttt tct gat gaa aca aat aca gag act ctc tac ggc acc tca ccc	360
Asp Phe Ser Asp Glu Thr Asn Thr Glu Thr Leu Tyr Gly Thr Ser Pro	
65 70 75	
cca agc aca cct cga cag atg aaa cgc ctg tca gcc aag cac cag agg	408
Pro Ser Thr Pro Arg Gln Met Lys Arg Leu Ser Ala Lys His Gln Arg	
80 85 90	
aac agc gca ggg agg ccg gcc agc cga tcg aac ttg aaa gaa aaa atg	456
Asn Ser Ala Gly Arg Pro Ala Ser Arg Ser Asn Leu Lys Glu Lys Met	
95 100 105 110	
aac aca ccg agt cag tct cca cat aaa gat ttg ggg aag gga gtg gag	504
Asn Thr Pro Ser Gln Ser Pro His Lys Asp Leu Gly Lys Gly Val Glu	
115 120 125	
acc gtg gaa gaa tac agc tac aag cag gag aag aag att cga gca act	552
Thr Val Glu Glu Tyr Ser Tyr Lys Gln Glu Lys Lys Ile Arg Ala Thr	
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ctg aga aca acg gag cga gac cat aag aaa aat gca cag tgc tca ttc	600
Leu Arg Thr Thr Glu Arg Asp His Lys Lys Asn Ala Gln Cys Ser Phe	
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Met Leu Asp Ser Val Ala Gly Ser Leu Pro Lys Lys Ser Ile Pro Asp	
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gtg gat ctc aat aag cct tac ctc agt ctc ggc tgt agc aat gcc aag	696
Val Asp Leu Asn Lys Pro Tyr Leu Ser Leu Gly Cys Ser Asn Ala Lys	
175 180 185 190	
ctg ccc gtc tcg atg ccc atg ccg ata gcc aga act gca cgg cag act	744
Leu Pro Val Ser Met Pro Met Pro Ile Ala Arg Thr Ala Arg Gln Thr	
195 200 205	
tcc cgg act gac tgc ccc gca gat cgc tta aag ttc ttt gaa aca ctg	792
Ser Arg Thr Asp Cys Pro Ala Asp Arg Leu Lys Phe Phe Glu Thr Leu	
210 215 220	
cgc ctt ttg cta aag ctt acc tca gtc tcg aag aag aag gac agg gag	840
Arg Leu Leu Leu Lys Leu Thr Ser Val Ser Lys Lys Lys Asp Arg Glu	
225 230 235	
cag agg gga caa gaa aac acg gct gct ttc tgg ttc aac cga tcg aac	888
Gln Arg Gly Gln Glu Asn Thr Ala Ala Phe Trp Phe Asn Arg Ser Asn	
240 245 250	
gaa ctg atc tgg tta gaa ctg cag gcc tgg cac gcg ggc cgc acc atc	936
Glu Leu Ile Trp Leu Glu Leu Gln Ala Trp His Ala Gly Arg Thr Ile	
255 260 265 270	
aat gac cag gac ctc ttt ctc tac aca gcc cgc cag gcc atc cca gac	984
Asn Asp Gln Asp Leu Phe Leu Tyr Thr Ala Arg Gln Ala Ile Pro Asp	
275 280 285	
atc atc aat gag atc ctc acc ttc aaa gtt aac tac ggg agc att gcc	1032
Ile Ile Asn Glu Ile Leu Thr Phe Lys Val Asn Tyr Gly Ser Ile Ala	
290 295 300	

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 35 40 45

Leu Gly Glu Ser Ala Arg Lys Ser Met Glu Ser Asp Pro Glu Asp Phe
 50 55 60

Ser Asp Glu Thr Asn Thr Glu Thr Leu Tyr Gly Thr Ser Pro Pro Ser
 65 70 75 80

Thr Pro Arg Gln Met Lys Arg Leu Ser Ala Lys His Gln Arg Asn Ser
 85 90 95

Ala Gly Arg Pro Ala Ser Arg Ser Asn Leu Lys Glu Lys Met Asn Thr
 100 105 110

Pro Ser Gln Ser Pro His Lys Asp Leu Gly Lys Gly Val Glu Thr Val
 115 120 125

Glu Glu Tyr Ser Tyr Lys Gln Glu Lys Lys Ile Arg Ala Thr Leu Arg
 130 135 140

Thr Thr Glu Arg Asp His Lys Lys Asn Ala Gln Cys Ser Phe Met Leu
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Asp Ser Val Ala Gly Ser Leu Pro Lys Lys Ser Ile Pro Asp Val Asp
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Leu Asn Lys Pro Tyr Leu Ser Leu Gly Cys Ser Asn Ala Lys Leu Pro
 180 185 190

Val Ser Met Pro Met Pro Ile Ala Arg Thr Ala Arg Gln Thr Ser Arg
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Thr Asp Cys Pro Ala Asp Arg Leu Lys Phe Phe Glu Thr Leu Arg Leu
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Leu Leu Lys Leu Thr Ser Val Ser Lys Lys Lys Asp Arg Glu Gln Arg
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Gly Gln Glu Asn Thr Ala Ala Phe Trp Phe Asn Arg Ser Asn Glu Leu
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Ile Trp Leu Glu Leu Gln Ala Trp His Ala Gly Arg Thr Ile Asn Asp
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Gln Asp Leu Phe Leu Tyr Thr Ala Arg Gln Ala Ile Pro Asp Ile Ile
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Ser Asn Gly Ala Gly Phe Asn Gly Pro Leu Val Glu Gly Gln Cys Arg

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Lys Asp Tyr Glu Arg Tyr Ala Ala Lys Asp Phe Glu Asp Arg Val Gln						
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Arg Ile Met Gly Thr Val Leu Gly Ile Lys Asn Leu Ser Asp Ile Gly						
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Trp Pro Val Phe Glu Ile Pro Ser Pro Arg Pro Ser Lys Gly Tyr Glu						
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Pro Glu Asp Glu Val Glu Asp Thr Glu Val Glu Leu Arg Glu Leu Glu						
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Ser Gly Thr Glu Glu Ser Asp Glu Glu Pro Thr Pro Ser Pro Arg Val						
		450		455		460
Pro Glu Leu Arg Leu Ser Thr Asp Thr Ile Leu Asp Ser Arg Ser Gln						
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Ile Gly Trp Gly Thr Ala Asp Cys Gly Pro Glu Ala Ser Arg His Cys						
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Leu Thr Ser Ile Tyr Arg Pro Phe Val Asp Lys Ala Leu Lys Gln Met						
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Arg Leu Glu Gln Arg Pro Ala Gly Glu Pro Ser Leu Leu Ser Ile Lys						
		625		630		635
Gln Leu Val Arg Glu Cys Lys Glu Val Leu Lys Gly Gly Leu Leu Met						
		645		650		655
Lys Gln Tyr Tyr Gln Phe Met Leu Gln Glu Val Leu Gly Gly Leu Glu						
		660		665		670

Lys Thr Asp Cys Asn Met Asp Ala Phe Glu Glu Asp Leu Gln Lys Met
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 Cys Ser Val Lys Leu Lys Asn Asn Ala Gln Thr Met Pro Gly Glu Val
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 Asn Ser Thr Leu Gly Thr Ala Ala Tyr Met Ala Pro Glu Val Ile Thr
 1490 1495 1500
 Arg Ala Lys Gly Glu Gly His Gly Arg Ala Ala Asp Ile Trp Ser Leu
 505 1510 1515 1520
 Gly Cys Val Val Ile Glu Met Val Thr Gly Lys Arg Pro Trp His Glu
 1525 1530 1535
 Tyr Glu His Asn Phe Gln Ile Met Tyr Lys Val Gly Met Gly His Lys
 1540 1545 1550
 Pro Pro Ile Pro Glu Arg Leu Ser Pro Glu Gly Lys Ala Phe Leu Ser
 1555 1560 1565
 His Cys Leu Glu Ser Asp Pro Lys Ile Arg Trp Thr Ala Ser Gln Leu
 1570 1575 1580
 Leu Asp His Ala Phe Val Lys Val Cys Thr Asp Glu Glu
 585 1590 1595
 <210> 15
 <211> 20
 <212> PRT
 <213> synthetic construct
 <400> 15
 Ile Ile Gly Glu Val Cys Asp Thr Pro Lys Ser Tyr Asp Arg Val Met 16
 1 5 10 15
 His Val Gly Leu Arg
 20
 <210> 16
 <211> 14
 <212> PRT
 <213> synthetic construct
 <400> 16
 <220>
 <223> Xaa at postions 3, 5, 6, 8, 10 and 11 = any amino acid
 Ile Ser Xaa Pro Xaa Xaa Phe Xaa His Xaa Xaa His Val Gly
 1 5 10
 <210> 17
 <211> 20
 <212> DNA
 <213> synthetic construct

<220>
 <223> N at postion 4 = c or t

 <220>
 <223> N at postions 6,12,and 15 = Inosine

 <400> 17
 garntnatgg cngtnaarca 20

 <210> 18
 <211> 23
 <212> DNA
 <213> synthetic construct

 <220>
 <223> N at postions 3,6,12,and 18 = Inosine

 <220>
 <223> N at postion 9 = t or c

 <220>
 <223> N at postion 20 = g or t

 <400> 18
 ttngcncnt tnatrtcnen rtg 23

 <210> 19
 <211> 11
 <212> PRT
 <213> synthetic construct

 <400> 19
 Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
 1 5 10

 <210> 20
 <211> 56
 <212> DNA
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 <400> 20
 atgggggtacc cgtacgacgt gccggactac gcttccgatg atcagcaagc tttgaa 56

 <210> 21
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 <212> DNA
 <213> synthetic construct

 <400> 21
 atgggggtacc cgtacgacgt gccggactac gcttccgatg aacaagaggc attaga 56

 <210> 22
 <211> 21
 <212> DNA
 <213> synthetic construct

 <400> 22
 agacttagat ctcaggtett c 21

 <210> 23
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<212> DNA
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<400> 23
 gattctgacg tcactctgcc t 21

<210> 24
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 <212> DNA
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<400> 24
 tcacgttcta gagccaccat ggggtacccg tacga 35

<210> 25
 <211> 19
 <212> PRT
 <213> synthetic construct

<400> 25
 Cys Glu Ala Arg Gln Arg Pro Ser Ala Glu Glu Leu Leu Thr His His
 1 5 10 15

Phe Ala Gln

<210> 26
 <211> 14
 <212> PRT
 <213> synthetic construct

<400> 26
 Cys Phe Val Phe Pro Pro Leu Asp Gln Glu Glu Met Glu Ser
 1 5 10

<210> 27
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 <212> PRT
 <213> synthetic construct

<400> 27
 Thr Thr Tyr Ala Asp Phe Ile Ala Ser Gly Arg Thr Gly Arg Arg Asn
 1 5 10 15

Ala Ile His Asp
 20